CLAIMS

1. A method for determining the quality, expressed in terms of a quality value, of an biomolecule sample, based on measured data of the biomolecule sample, wherein the method comprises the following steps:
extracting a number of prescribed features from the measured data using data analysis,
determining the quality value from the extracted features using a quality algorithm.

2. The method of claim 1, comprising at least one of the features:
one or more anomalous cases are specified from among a prescribed number of potentially anomalous cases,
a number of prescribed features are extracted from the measured data of the biomolecule sample using data analysis for every anomalous case,
the measured data is analyzed using an associated anomalous-case algorithm in order to validate every anomalous case identified, and
the magnitude of the anomaly involved is determined from a combination of the anomalous cases present in order to determine the degree to which the biomolecule sample is anomalous.

3. The method of claim 1 or any one of the above claims, wherein the following steps are carried out in order to determine the quality algorithm:
collecting a statistically significant number of trial measured data covering a prescribed set of biomolecule samples,
assigning a quality label to every measured data,
extracting features from the measured data using data analysis,
determining functional interrelations among the quality labels and one or more combinations of the extracted features,
assigning a rating factor to every functional interrelation, and
specifying the functional interrelation that has the highest rating factor as the quality algorithm.

4. The method of claim 3, wherein the functional interrelations among the quality labels and the various combinations of extracted features are determined using an adaptive approach.

5. The method of claim 2, wherein the following steps are carried out in order to determine the anomalous-case algorithm for a prescribed anomalous case:
collecting a statistically significant number of trial measured data covering a prescribed set of biomolecule samples,
assigning an anomalous-case label to the prescribed anomalous case of every measured data,
extracting features from the measured data using data analysis,
determining functional interrelations among the anomalous-case labels and one or more combinations of the extracted features,
assigning a rating factor to every functional interrelation, and
specifying the function interrelation that has the highest rating factor as the anomalous-case algorithm.

6. The method of claim 5, wherein the functional interrelations among the anomalous-case labels and the various combinations of extracted features are determined using an adaptive approach.

7. The method of claim 3 or 4, wherein discrete classes are established for the accessible range of measured data quality and every class is assigned a quality label.

8. The method of claim 7, wherein seven classes are established for the quality label.

9. The method of claim 5 or 6, wherein 0 and 1 are prescribed as allowed values of the anomalous-case label.

10. The method –of claim 1 or any one of the above claims, wherein the measured data are subdivided into segments in order to extract features therefrom.

11. The method of claim 10, wherein the biomolecule sample is an RNA sample, and the following eight regions of the measured data of the RNA sample are established as segments: a preregion, a marker region, a 5S-region, a fast region, an 18S-region, an interregion, a 28S-region, and a postregion.

12. The method of claim 3 or any one of the above claims, wherein the positions, heights, and widths of peaks occurring in the measured data are determined and their areas computed by integration under the data analysis performed on the measured data.

13. The method of claim 10 or 11, wherein the following local features of segments of the data curve, or smoothed data curve, of the measured data are determined in the data analysis of the measured data: the maximum and minimum value occurring within the segment, the slope and y-intercept of the interpolating straight line fitted to the points on the curve falling within the bounds of the segment, the y-values of this interpolating straight line at the start and end points of the segment, the area under the curve, the area under the interpolating straight line, the ratios of the latter areas to the area under the entire data curve, the deviation of the interpolating straight line from the data curve, and/or the deviations of the original and smoothed data curve from one another.

14. The method of claim 13, wherein Savitzky-Golay filters and/or the rolling-ball algorithm are employed for smoothing the data curve.

15. The method of claim 10 or any one of the above claims, wherein the biomolecule sample is an RNA sample, and the following global features are determined in the data analysis of the measured data: the ratio of the areas of the 18S-fragment and 28S-fragment to the total area enclosed within the utilized section, the ratio of the area of the 18S-fragment to the area of the 28S-fragment, and/or the signal/noise ratio.

16. The method of claim 3 or any one of the above claims, wherein the extracted features are consecutively arranged in a list such that the information on the

quality label and/or anomalous-case label will be progressively maximized as each additional feature is added, where each addition of a feature to the list defines a new combination of features.

17. The method of claim 16, wherein the arrangement of extracted features in the list is based on mutual information.

18. The method of claim 4 or 6, wherein a neural network is employed as the adaptive approach.

19. The method of claim 18, wherein a Bayesian method is applied for adjusting parameters for the neural network.

20. The method of claim 18 or 19, wherein functional interrelations of varying complexity are determined, where the necessary complexity of the functional interrelations sought is obtained by iterative additions of hidden neurons to the neuronal network.

21. The method of claim 19, wherein the *a-posteriori* probability of the neuronal network computed using a Bayesian method is employed as rating factor.

22. The method of claim 1 or any one of the above claims, wherein the biomolecule sample comprises at least one of a group comprising: an RNA sample, a DNA sample, a protein sample, a peptide sample, a sugar sample, a lipid sample, and a modified form of one or more of the aforementioned biomolecule samples.

23. The method of claim 1 or any one of the above claims, wherein the biomolecule sample comprises representatives of one or more of the known biomolecule types, such as RNA molecules, DNA molecules, protein molecules, peptides, sugars, or lipids, including modified forms of the former biomolecules.

24. The method of claim 1 or any one of the above claims, wherein the quality value is a measure of the biomolecular sample's integrity.

25. The method of claim 1 or any one of the above claims, wherein the measured data is an electropherogram.

26. A method for determining the quality, expressed in terms of a quality value, of an RNA sample, based on an electropherogram of the RNA sample,
wherein the method comprises the following steps:
extracting a number of prescribed features from the electropherogram using data analysis,
determining the quality value from the extracted features using a quality algorithm.

27. A software program or product, preferably stored on a data carrier, for executing the method of claim 1 or any one of the above claims, when run on a data processing system such as a computer.

28. An apparatus for determining the quality, expressed in terms of a quality value, of an biomolecule sample, based on measured data of the biomolecule sample, the apparatus comprising:

a processing unit adapted for extracting a number of prescribed features from the measured data using data analysis, and for determining the quality value from the extracted features using a quality algorithm.